

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: HIRANO, TOSHIO
KAISHO, TSUNEYASU
- (ii) TITLE OF INVENTION: MEMBRANE PROTEIN POLYPEPTIDE HAVING
PRE-B CELL GROWTH-SUPPORTING ABILITY AND A GENE THEREOF
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
(B) STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
(C) CITY: ARLINGTON
(D) STATE: VA
(E) COUNTRY: USA
(F) ZIP: 22202
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/624,650
(B) FILING DATE: 22-MAY-1996
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/JP94/01732
(B) FILING DATE: 14-OCT-1994
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: JP 5-281622
(B) FILING DATE: 15-OCT-1993
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: OBLON, NORMAN F.
(B) REGISTRATION NUMBER: 24,618
(C) REFERENCE/DOCKET NUMBER: 7625-001-0 PCT
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 703-413-3000
(B) TELEFAX: 703-413-2220

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 amino acids

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 996 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGGAATTCA TGGCATCTAC TTCGTATGAC TATTGCAGAG TGCCCATGGA AGACGGGGAT	60
AAGCGCTGTA AGCTTCTGCT GGGGATAGGA ATTCTGGTGC TCCTGATCAT CGTGATTCTG	120
GGGGTGCCCT TGATTATCTT CACCATCAAG GCCAACAGCG AGGCCTGCCG GGACGGCCTT	180
CGGGCAGTGA TGGAGTGTCT CAATGTCACC CATCTCCTGC AACAAAGAGCT GACCGAGGCC	240
CAGAAGGGCT TTCAGGATGT GGAGGCCCAG GCGCCACCT GCAACCACAC TGTGATGGCC	300
CTAATGGCTT CCCTGGATGC AGAGAAGGCC CAAGGACAAA AGAAAAGTGA GGAGCTTGAG	360
GGAGAGATCA CTACATTAAT CCATAAGCTT CAGGACGCGT CTGCAGAGGT GGAGCGACTG	420
AGAAGAGAAA ACCAGGTCTT AAGCGTGAGA ATCGCGGACA AGAAGTACTA CCCAGCTCC	480
CAGGACTCCA GCTCCGCTGC GCGCGCCCAG CTGCTGATTG TGCTGCTGGG CCTCAGCGCT	540
CTGCTGCAGT GAGATCCCAG GAAGCTGGCA CATCTTGAA GGTCCGTCCT GCTCGGCTTT	600
TGCTTGAAC ATTCCCTTGA TCTCATCAGT TCTGAGCGGG TCATGGGGCA ACACGGTTAG	660
CGGGGAGAGC ACGGGGTAGC CGGAGAAGGG CCTCTGGAGC AGGTCTGGAG GGGCCATGGG	720
GCAGTCCTGG GTGTGGGGAC ACAGTCGGGT TGACCCAGGG CTGTCTCCCT CCAGAGCCTC	780
CCTCCGGACA ATGAGTCCCC CCTCTGTCT CCCACCTGA GATTGGGCAT GGGGTGCGGT	840
GTGGGGGGCA TGTGCTGCCT GTTGTTATGG GTTTTTTTT CGGGGGGGGT TGCTTTTTTC	900
TGGGTCTTT GAGCTCCAAA AAATAAACAC TTCCTTTGAG GGAGAGCAAA AAAAAAAAAA	960
AAAAAAAAAA AAAAAAAAAA AAAGAATTCC ACCACA	996

Figure 1 illustrates the steps of the proposed algorithm for finding the minimum spanning tree of a graph. The process starts with a graph (a) and proceeds through steps (b) to (l), showing the selection of edges and the resulting partial spanning trees. The final result is the minimum spanning tree (l).

SEQUENCE DESCRIPTION:

- 3 3 -

SEQ ID NO: 2
 SEQUENCE LENGTH: 996
 SEQUENCE TYPE: Nucleic acid
 STRANDEDNESS: Double
 TOPOLOGY: Linear
 MOLECULE TYPE: cDNA to mRNA
 METHOD FOR DETERMINING FEATURES: E
 SEQUENCE DESCRIPTION:

GTGGAATTC ATG GCA TCT ACT TCG TAT GAC TAT TGC AGA GTG CCC ATG GAA 51
 GAC GGG GAT AAG CGC TGT AAG CTT CTG CTG GGG ATA GGA ATT CTG GTG 99
 CTC CTG ATC ATC GTG ATT CTG GGG GTG CCC TTG ATT ATC TTC ACC ATC 147
 AAG GCC AAC AGC GAG GCC TGC CGG GAC GGC CTT CGG GCA GTG ATG GAG 195
 TGT CGC AAT GTC ACC CAT CTC CTG CAA CAA GAG CTG ACC GAG GCC CAG 243
 AAG GGC TTT CAG GAT GTG GAG GCC CAG GCC GCC ACC TGC AAC CAC ACT 291
 GTG ATG GCC CTA ATG GCT TCC CTG GAT GCA GAG AAG GCC CAA GGA CAA 339
 AAG AAA GTG GAG GAG CTT GAG GGA GAG ATC ACT ACA TTA AAC CAT AAG 387
 CTT CAG GAC GCG TCT GCA GAG GTG GAG CGA CTG AGA AGA GAA AAC CAG 435
 GTC TTA AGC GTG AGA ATC GCG GAC AAG AAG TAC TAC CCC AGC TCC CAG 483
 GAC TCC AGC TCC GCT GCG GCG CCC CAG CTG CTG ATT GTG CTG CTG GGC 531
 CTC AGC GCT CTG CTG CAG TGAGATCCCA GGAAGCTGGC ACATCTTGGA AGGTCCGTC 589
 TGCTCGGCTT TTCGCTTGAA CATTCCCTTG ATCTCATCAG TTCTGAGCGG GTCATGGGGC 649
 AACACGGTTA GCGGGGAGAG CACGGGGTAG CCGGAGAAGG GCCTCTGGAG CAGGCTGGA 709
 GGGGCCATGG GGCAGTCCTG GGTGTGGGA CACAGTCGGG TTGACCCAGG GCTGTCTCCC 769
 TCCAGAGCCT CCTCCGGAC AATGAGTCCC CCTCTTTGTC TCCCACCTG AGATTGGGCA 829
 TGGGGTGGCG TGTGGGGGGC ATGTGCTGCC TGTGTTATG GGTTTTTTTT GCGGGGGGGG 889
 TTGCTTTTTT CTGGGGTCTT TGAGCTCCAA AAAATAAACA CTTCCTTGA GGGAGAGCAA 949
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAGAATTC CACCACA 996